

Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1. (Withdrawn) A method for comparing a query peptide to a plurality of database peptides comprising the steps of:
 - (a) constructing an index table, said index table comprising a plurality of records corresponding to a plurality of allowed mass values, said records comprising zero or more fields, said constructing step comprising the steps of:
 - (i) selecting a first peptide from said plurality of database peptides;
 - (ii) calculating a plurality of associated masses for said first peptide;
 - (iii) selecting a first associated mass from said plurality of associated masses;
 - (iv) referencing a first record from said plurality of records, said first record corresponding to said first associated mass;
 - (v) entering a first field into said first record, said first field comprising a first peptide index referencing said first peptide;
 - (vi) repeating steps (iii)-(v) for at least one other associated mass from said plurality of associated masses;
 - (vii) repeating steps (i)-(vi) for at least one other peptide from said plurality of database peptides; and
 - (b) generating a plurality of comparison scores, said plurality of comparison scores corresponding to said plurality of database peptides, said generating step comprising the steps of:
 - (i) generating a plurality of query mass values for said query peptide;
 - (ii) selecting a first query mass value from said plurality of query mass values;
 - (iii) referencing a second record from said plurality of records, said second record corresponding to said first query mass value;

- (iv) selecting a second field from said second record, said second field comprising a second peptide index;
 - (v) selecting a first comparison score from said plurality of comparison scores, said first comparison score corresponding to said second peptide index;
 - (vi) incrementing said first comparison score;
 - (vii) repeating steps (ii)-(vi) for at least one other query mass value selected from said plurality of query mass values.
2. (Withdrawn) The method of claim 1 wherein said generating step (b)(i) comprises the step of performing mass spectroscopy on said query peptide.
3. (Withdrawn) The method of claim 2 wherein said mass spectroscopy is performed by a method selected from the set consisting of: Fourier transform ion cyclotron resonance ("FTICR"), quadrupole mass spectroscopy, ion trap mass spectroscopy, and time-of-flight mass spectroscopy.
4. (Withdrawn) The method of claim 1 wherein said calculating step (a)(ii) comprises the step of calculating a plurality of associated masses for said first peptide, said plurality of associated masses comprising a plurality of primary masses and a plurality of complementary masses.
5. (Withdrawn) The method of claim 1 wherein said generating step (b) further comprises the step of multiplying said first comparison score by a weight value, wherein said weight value is a function of the type of mass value.
6. (Withdrawn) The method of claim 5 wherein said type of mass value is selected from the group consisting of: y-ion, b-ion, peak mass, and complementary mass.
7. (Withdrawn) A method for comparing a query peptide to a plurality of database peptides comprising the steps of:

- (a) constructing a first index table, said first index table comprising a first plurality of records corresponding to a plurality of allowed mass values, said records comprising zero or more fields; and
 - (b) constructing a second index table, said second index table comprising a second plurality of records corresponding to said plurality of allowed mass values, said records comprising zero or more fields; and
 - (c) calculating a plurality weight values, said weight values set according to the predictive value of said first and second index tables.
8. (Currently Amended) A method for comparing a modified query peptide to a plurality of database peptides comprising the steps of:
- (a) generating a plurality of query mass values for said modified query peptide;
 - (b) identifying a set of [~~query~~] modified mass values from said plurality of query mass values[~~, wherein said set corresponds to modified mass values~~];
 - (c) determining a spectral range for said modified query peptide;
 - (d) subdividing said spectral range into a plurality of mass [~~equal~~] intervals; and
 - (e) performing a plurality of searches on said plurality of mass [~~equal~~] intervals comparing the modified query peptide to the plurality of database peptides.
9. (Currently Amended) The method of claim 8 further comprising the step of excluding said [~~set of query~~] modified mass values during the comparison of the modified query peptide to the plurality of database peptides.
10. (Currently Amended) The method of claim 8 further comprising the step of adjusting said [~~set of query~~] modified mass values during the comparison of the modified query peptide to the plurality of database peptides.
11. (Withdrawn) A method for comparing a query peptide to a plurality of database peptides comprising the step of constructing an index table, said index table comprising a plurality of records corresponding to a plurality of allowed mass values, said records comprising zero or more fields, said constructing step comprising the steps of:

- (i) selecting a first peptide from said plurality of database peptides;
 - (ii) identifying a modification site on said first peptide;
 - (iii) applying a modification to said modification site, producing a first modified peptide;
 - (iv) calculating a plurality of associated masses for said first modified peptide;
 - (v) selecting a first associated mass from said plurality of associated masses;
 - (vi) referencing a first record from said plurality of records, said first record corresponding to said first associated mass;
 - (vii) entering a first field into said first record, said first field comprising a first peptide index referencing said first peptide;
 - (viii) repeating steps (v)-(vii) for at least one other associated mass from said plurality of associated masses;
 - (ix) repeating steps (i)-(viii) for at least one other peptide from said plurality of database peptides.
12. (Currently Amended) The method of claim [11] 8 wherein ~~[said identification step (ii) comprises the step of identifying]~~ the modified mass value corresponds to a modification site selected from the group consisting of: a phosphorylation site, an oxidation site, and a substitution site.
13. (Original) The method of claim 12 wherein said phosphorylation site comprises an amino acid selected from the group consisting of: serine, threonine, and tyrosine.
14. (Original) The method of claim 12 wherein said oxidation site comprises an amino acid selected from the group consisting of: cysteine and methionine.
15. (Original) The method of claim 12 wherein said substitution site comprises an amino acid selected from the group consisting of: glutamine, glutamate, asparagine, and aspartate.
16. (New) The method of claim 8 wherein the spectral range of the modified query peptide has a value from zero to the unmodified query peptides mass.

17. (New) The method of claim 8 wherein a selected comparison between the modified query peptide and the plurality of database peptides further identifies modified mass values for the modified query peptide that reside within the mass interval of the selected comparison.
18. (New) The method of claim 8 further comprising collectively evaluating the comparisons of the modified query peptide to the plurality of database peptides to identify a best match between the modified query peptide and the plurality of database peptides.
19. (New) The method of claim 8 further comprising collectively evaluating the comparisons of the modified query peptide to the plurality of database peptides to determine the putative identity of the modified query peptide.